AMENDMENT TO THE CLAIMS

Please cancel Claims 5-17 and 20-21 without prejudice and amend Claims 1, 3 and 19 as shown in the following listing of the claims:

1. (Currently amended) A method for determining whether a HIV-1 has an increased likelihood of being hypersusceptible to treatment with ~~a protease inhibitor~~ amprenavir, comprising: detecting whether the protease encoded by said HIV exhibits the presence or absence of a mutation associated with hypersusceptibility to treatment with ~~said protease inhibitor~~ amprenavir at amino acid position corresponding to position ~~16, 20, 33, 36, 37,~~ 39, ~~45,~~ 65, 69, ~~77,~~ or 89 ~~or 93 of an amino acid sequence of said protease~~ of SEQ ID NO:1, wherein the mutation at amino acid position corresponding to position 39 of SEQ ID NO:1 is S, the mutation at amino acid position corresponding to position 65 of SEQ ID NO:1 is D, the mutation at amino acid position corresponding to position 69 of SEQ ID NO:1 is K, and the mutation at amino acid position corresponding to position 89 of SEQ ID NO:1 is M, and wherein the presence of said mutation indicates that the HIV has an increased likelihood of being hypersusceptible to treatment with ~~the protease inhibitor, with the proviso that said mutation is not L33F~~ amprenavir.

2. (Original) The method of claim 1, wherein the protease has a sequence that is greater than 80% identical to SEQ ID NO:1.

3. (Currently amended) A method for determining whether an individual infected with HIV-1 has an increased likelihood of being hypersusceptible to treatment with ~~a protease inhibitor~~ amprenavir, comprising detecting, in a sample from said individual, the presence or absence of a mutation associated with hypersusceptibility to treatment with ~~a protease inhibitor~~ amprenavir at amino acid position corresponding to position ~~16, 20, 33, 36, 37,~~ 39, ~~45,~~ 65, 69, ~~77,~~ or 89 ~~or 93 of an amino acid sequence of said protease~~ of SEQ ID NO:1, wherein the mutation at amino acid position corresponding to position 39 of SEQ ID NO:1 is S, the mutation at amino acid position corresponding to position 65 of SEQ ID NO:1 is D, the mutation at amino acid position corresponding to position 69 of SEQ ID NO:1 is K, and the mutation at amino acid position corresponding to position 89 of SEQ ID NO:1 is M, and wherein the presence of said mutation indicates that the individual has an increased likelihood of being hypersusceptible to treatment with ~~the protease inhibitor, with the proviso that said mutation is not L33F~~ amprenavir.

4. (Original) The method of claim 3, wherein the protease has a sequence that is greater than 80% identical to SEQ ID NO:1.

5.-17. (Canceled).

18. (Original) The method of claim 3, wherein the individual is undergoing or has undergone prior treatment with an anti-viral drug.

19. (Currently amended) The method of claim 1, wherein the method comprises detecting the presence or absence of a mutation associated with hypersusceptibility to treatment with ~~said protease~~ inhibitor at at least 2, 3~~, 4, 5, 6, 7, 8, 9, 10, 11 or 12~~ or 4 of the amino acid positions.

20.-21. (Canceled).